#2

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RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/073,054

DATE: 03/01/2002
TIME: 10:52:16

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Output Set: N:\CRF3\03012002\J073054.raw

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 3 <110> APPLICANT: Garvan Institute of Medical Research
 4       HERZOG, Herbert
 6 <120> TITLE OF INVENTION: Novel G-protein coupled receptor-encoding gene and
diagnostic uses
 7       therefor
 9 <130> FILE REFERENCE: 1871-132 (93702-CIP/MRO)
C--> 11 <140> CURRENT APPLICATION NUMBER: US/10/073,054
C--> 11 <141> CURRENT FILING DATE: 2002-02-12
 11 <150> PRIOR APPLICATION NUMBER: US 09/308,696
 12 <151> PRIOR FILING DATE: 1999-06-11
 14 <150> PRIOR APPLICATION NUMBER: PCT/AU98/00805
 15 <151> PRIOR FILING DATE: 1998-09-24
 17 <150> PRIOR APPLICATION NUMBER: AU PO9386
 18 <151> PRIOR FILING DATE: 1997-09-24
 20 <160> NUMBER OF SEQ ID NOS: 20
 22 <170> SOFTWARE: PatentIn version 3.1
 24 <210> SEQ ID NO: 1
 25 <211> LENGTH: 2822
 26 <212> TYPE: DNA
 27 <213> ORGANISM: Human GPR56-1(TSR32)
 29 <220> FEATURE:
 30 <221> NAME/KEY: CDS
 31 <222> LOCATION: (163)..(2241)
 32 <223> OTHER INFORMATION:
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 40 attacaggtg gtgacttcca agagtgactc cgtcggagga aa atg act ccc cag       174
 41                                                   Met Thr Pro Gln
 42                                                    1
 44 tcg ctg ctg cag acg aca ctg ttc ctg ctg agt ctg ctc ttc ctg gtc     222
 45 Ser Leu Leu Gln Thr Thr Leu Phe Leu Leu Ser Leu Leu Phe Leu Val
 46  5               10                  15                  20
 48 caa ggt gcc cac ggc agg ggc cac agg gaa gac ttt cgc ttc tgc agc     270
 49 Gln Gly Ala His Gly Arg Gly His Arg Glu Asp Phe Arg Phe Cys Ser
 50                  25                  30                  35
 52 cag cgg aac cag aca cac agg agc agc ctc cac tac aaa ccc aca cca     318
 53 Gln Arg Asn Gln Thr His Arg Ser Ser Leu His Tyr Lys Pro Thr Pro
 54                  40                  45                  50
 56 gac ctg cgc atc tcc atc gag aac tcc gaa gag gcc ctc aca gtc cat     366
 57 Asp Leu Arg Ile Ser Ile Glu Asn Ser Glu Glu Ala Leu Thr Val His
 58          55                  60                  65
 60 gcc cct ttc cct gca gcc cac cct gct tcc cga tcc ttc cct gac ccc     414
 61 Ala Pro Phe Pro Ala Ala His Pro Ala Ser Arg Ser Phe Pro Asp Pro
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62     70                      75                      80
64 agg ggc ctc tac cac ttc tgc ctc tac tgg aac cga cat gct ggg aga     462
65 Arg Gly Leu Tyr His Phe Cys Leu Tyr Trp Asn Arg His Ala Gly Arg
66 85                      90                      95                     100
68 tta cat ctt ctc tat ggc aag cgt gac ttc ttg ctg agt gac aaa gcc     510
69 Leu His Leu Leu Tyr Gly Lys Arg Asp Phe Leu Leu Ser Asp Lys Ala
70                     105                     110                     115
72 tct agc ctc ctc tgc ttc cag cac cag gag gag agc ctg gct cag ggc     558
73 Ser Ser Leu Leu Cys Phe Gln His Gln Glu Glu Ser Leu Ala Gln Gly
74                 120                     125                     130
76 ccc ccg ctg tta gcc act tct gtc acc tcc tgg tgg agc cct cag aac     606
77 Pro Pro Leu Leu Ala Thr Ser Val Thr Ser Trp Trp Ser Pro Gln Asn
78             135                     140                     145
80 atc agc ctg ccc agt gcc gcc agc ttc acc ttc tcc ttc cac agt cct     654
81 Ile Ser Leu Pro Ser Ala Ala Ser Phe Thr Phe Ser Phe His Ser Pro
82         150                     155                     160
84 ccc cac acg gcc gct cac aat gcc tcg gtg gac atg tgc gag ctc aaa     702
85 Pro His Thr Ala Ala His Asn Ala Ser Val Asp Met Cys Glu Leu Lys
86 165                     170                     175                     180
88 agg gac ctc cag ctg ctc agc cag ttc ctg aag cat ccc cag aag gcc     750
89 Arg Asp Leu Gln Leu Leu Ser Gln Phe Leu Lys His Pro Gln Lys Ala
90                     185                     190                     195
92 tca agg agg ccc tcg gct gcc ccc gcc agc cag cag ttg cag agc ctg     798
93 Ser Arg Arg Pro Ser Ala Ala Pro Ala Ser Gln Gln Leu Gln Ser Leu
94                 200                     205                     210
96 gag tcg aaa ctg acc tct gtg aga ttc atg ggg gac atg gtg tcc ttc     846
97 Glu Ser Lys Leu Thr Ser Val Arg Phe Met Gly Asp Met Val Ser Phe
98             215                     220                     225
100 gag gag gac cgg atc aac gcc acg gta tgg aag ctc cag ccc aca gcc    894
101 Glu Glu Asp Arg Ile Asn Ala Thr Val Trp Lys Leu Gln Pro Thr Ala
102     230                     235                     240
104 ggc ctc cag gac ctg cac atc cac tcc cgg cag gag gag gag cag agc    942
105 Gly Leu Gln Asp Leu His Ile His Ser Arg Gln Glu Glu Glu Gln Ser
106 245                     250                     255                     260
108 gag atc atg gag tac tcg gtg ctg ctg cct cga aca ctc ttc cag agg    990
109 Glu Ile Met Glu Tyr Ser Val Leu Leu Pro Arg Thr Leu Phe Gln Arg
110                     265                     270                     275
112 acg aaa ggc cgg agc ggg gag gct gag aag aga ctc ctc ctg gtg gac   1038
113 Thr Lys Gly Arg Ser Gly Glu Ala Glu Lys Arg Leu Leu Leu Val Asp
114             280                     285                     290
116 ttc agc agc caa gcc ctg ttc cag gac aag aat tcc agc caa gtc ctg   1086
117 Phe Ser Ser Gln Ala Leu Phe Gln Asp Lys Asn Ser Ser Gln Val Leu
118             295                     300                     305
120 ggt gag aag gtc ttg ggg att gtg gta cag aac acc aaa gta gcc aac   1134
121 Gly Glu Lys Val Leu Gly Ile Val Val Gln Asn Thr Lys Val Ala Asn
122     310                     315                     320
124 ctc acg gag ccc gtg gtg ctc act ttc cag cac cag cta cag ccg aag   1182
125 Leu Thr Glu Pro Val Val Leu Thr Phe Gln His Gln Leu Gln Pro Lys
126 325                     330                     335                     340
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128 aat gtg act ctg caa tgt gtg ttc tgg gtt gaa gac ccc aca ttg agc    1230
129 Asn Val Thr Leu Gln Cys Val Phe Trp Val Glu Asp Pro Thr Leu Ser
130             345             350             355
132 agc ccg ggg cat tgg agc agt gct ggg tgt gag acc gtc agg aga gaa    1278
133 Ser Pro Gly His Trp Ser Ser Ala Gly Cys Glu Thr Val Arg Arg Glu
134             360             365             370
136 acc caa aca tcc tgc ttc tgc aac cac ttg acc tac ttt gca gtg ctg    1326
137 Thr Gln Thr Ser Cys Phe Cys Asn His Leu Thr Tyr Phe Ala Val Leu
138             375             380             385
140 atg gtc tcc tcg gtg gag gtg gac gcc gtg cac aag cac tac ctg agc    1374
141 Met Val Ser Ser Val Glu Val Asp Ala Val His Lys His Tyr Leu Ser
142     390             395             400
144 ctc ctc tcc tac gtg ggc tgt gtc gtc tct gcc ctg gcc tgc ctt gtc    1422
145 Leu Leu Ser Tyr Val Gly Cys Val Val Ser Ala Leu Ala Cys Leu Val
146 405             410             415             420
148 acc att gcc gcc tac ctc tgc tcc agg gtg ccc ctg ccg tgc agg agg    1470
149 Thr Ile Ala Ala Tyr Leu Cys Ser Arg Val Pro Leu Pro Cys Arg Arg
150             425             430             435
152 aaa cct cgg gac tac acc atc aag gtg cac atg aac ctg ctg ctg gcc    1518
153 Lys Pro Arg Asp Tyr Thr Ile Lys Val His Met Asn Leu Leu Leu Ala
154             440             445             450
156 gtc ttc ctg ctg gac acg agc ttc ctg ctc agc gag ccg gtg gcc ctg    1566
157 Val Phe Leu Leu Asp Thr Ser Phe Leu Leu Ser Glu Pro Val Ala Leu
158             455             460             465
160 aca ggc tct gag gct ggc tgc cga gcc agt gcc atc ttc ctg cac ttc    1614
161 Thr Gly Ser Glu Ala Gly Cys Arg Ala Ser Ala Ile Phe Leu His Phe
162     470             475             480
164 tcc ctg ctc acc tgc ctt tcc tgg atg ggc ctc gag ggg tac aac ctc    1662
165 Ser Leu Leu Thr Cys Leu Ser Trp Met Gly Leu Glu Gly Tyr Asn Leu
166 485             490             495             500
168 tac cga ctc gtg gtg gag gtc ttt ggc acc tat gtc cct ggc tac cta    1710
169 Tyr Arg Leu Val Val Glu Val Phe Gly Thr Tyr Val Pro Gly Tyr Leu
170             505             510             515
172 ctc aag ctg agc gcc atg ggc tgg ggc ttc ccc atc ttt ctg gtg acg    1758
173 Leu Lys Leu Ser Ala Met Gly Trp Gly Phe Pro Ile Phe Leu Val Thr
174             520             525             530
176 ctg gtg gcc ctg gtg gat gtg gac aac tat ggc ccc atc atc ttg gct    1806
177 Leu Val Ala Leu Val Asp Val Asp Asn Tyr Gly Pro Ile Ile Leu Ala
178             535             540             545
180 gtg cat agg act cca gag ggc gtc atc tac cct tcc atg tgc tgg atc    1854
181 Val His Arg Thr Pro Glu Gly Val Ile Tyr Pro Ser Met Cys Trp Ile
182     550             555             560
184 cgg gac tcc ctg gtc agc tac atc acc aac ctg ggc ctc ttc agc ctg    1902
185 Arg Asp Ser Leu Val Ser Tyr Ile Thr Asn Leu Gly Leu Phe Ser Leu
186 565             570             575             580
188 gtg ttt ctg ttc aac atg gcc atg cta gcc acc atg gtg gtg cag atc    1950
189 Val Phe Leu Phe Asn Met Ala Met Leu Ala Thr Met Val Val Gln Ile
190             585             590             595
192 ctg cgg ctg cgc ccc cac acc caa aag tgg tca cat gtg ctg aca ctg    1998
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193 Leu Arg Leu Arg Pro His Thr Gln Lys Trp Ser His Val Leu Thr Leu
194         600                 605                 610
196 ctg ggc ctc agc ctg gtc ctt ggc ctg ccc tgg gcc ttg atc ttc ttc     2046
197 Leu Gly Leu Ser Leu Val Leu Gly Leu Pro Trp Ala Leu Ile Phe Phe
198         615                 620                 625
200 tcc ttt gct tct ggc acc ttc cag ctt gtc gtc ctc tac ctt ttc agc     2094
201 Ser Phe Ala Ser Gly Thr Phe Gln Leu Val Val Leu Tyr Leu Phe Ser
202         630                 635                 640
204 atc atc acc tcc ttc caa ggc ttc ctc atc ttc atc tgg tac tgg tcc     2142
205 Ile Ile Thr Ser Phe Gln Gly Phe Leu Ile Phe Ile Trp Tyr Trp Ser
206 645                 650                 655                 660
208 atg cgg ctg cag gcc cgg ggt ggc ccc tcc cct ctg aag agc aac tca     2190
209 Met Arg Leu Gln Ala Arg Gly Gly Pro Ser Pro Leu Lys Ser Asn Ser
210         665                 670                 675
212 gac tgc gcc agg ctc ccc atc agc tcg ggc agc acc tcg tcc agc cgc     2238
213 Asp Cys Ala Arg Leu Pro Ile Ser Ser Gly Ser Thr Ser Ser Ser Arg
214         680                 685                 690
216 atc taggcctcca gcccacctgc ccatgtgatg aagcagagat gcggcctcgt          2291
217 Ile
220 cgcacactgc ctgtggcccc cgagccaggc ccagccccag gccagtcagc cgcagacttt     2351
222 ggaaagccca cgaccatggg agagatgggc cgttgccatg gtggacggac tcccgggggct     2411
224 ggggctttg aattggcctt ggggactact cggctctcac tcagctccca cgggactcag       2471
226 aagtgcgccg ccatgctgcc tagggtactg tccccacatc tgtcccaacc cagctggagg       2531
228 cctggtctct ccttacaacc cctgggccca gcctcattgc tggggggccag gccttggatc     2591
230 ttgagggtct ggcacatcct taatcctgtg cccctgcctg ggacagaaat gtggctccag       2651
232 ttgctctgtc tctcgtggtc accctgaggg cactctgcat cctctgtcat tttaacctca       2711
234 ggtggcaccc agggcgaatg gggcccaggg cagaccttca gggccagagc cctggcggag       2771
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240 <211> LENGTH: 693
241 <212> TYPE: PRT
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251         20                  25                  30
254 Arg Phe Cys Ser Gln Arg Asn Gln Thr His Arg Ser Ser Leu His Tyr
255         35                  40                  45
258 Lys Pro Thr Pro Asp Leu Arg Ile Ser Ile Glu Asn Ser Glu Glu Ala
259     50                  55                  60
262 Leu Thr Val His Ala Pro Phe Pro Ala Ala His Pro Ala Ser Arg Ser
263 65                  70                  75                  80
266 Phe Pro Asp Pro Arg Gly Leu Tyr His Phe Cys Leu Tyr Trp Asn Arg
267             85                  90                  95
270 His Ala Gly Arg Leu His Leu Leu Tyr Gly Lys Arg Asp Phe Leu Leu
271             100                 105                 110
274 Ser Asp Lys Ala Ser Ser Leu Leu Cys Phe Gln His Gln Glu Glu Ser
275         115                 120                 125
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278 Leu Ala Gln Gly Pro Pro Leu Leu Ala Thr Ser Val Thr Ser Trp Trp
279         130             135             140
282 Ser Pro Gln Asn Ile Ser Leu Pro Ser Ala Ala Ser Phe Thr Phe Ser
283 145             150             155             160
286 Phe His Ser Pro Pro His Thr Ala Ala His Asn Ala Ser Val Asp Met
287             165             170             175
290 Cys Glu Leu Lys Arg Asp Leu Gln Leu Leu Ser Gln Phe Leu Lys His
291         180             185             190
294 Pro Gln Lys Ala Ser Arg Arg Pro Ser Ala Ala Pro Ala Ser Gln Gln
295         195             200             205
298 Leu Gln Ser Leu Glu Ser Lys Leu Thr Ser Val Arg Phe Met Gly Asp
299         210             215             220
302 Met Val Ser Phe Glu Glu Asp Arg Ile Asn Ala Thr Val Trp Lys Leu
303 225             230             235             240
306 Gln Pro Thr Ala Gly Leu Gln Asp Leu His Ile His Ser Arg Gln Glu
307             245             250   ·         255
310 Glu Glu Gln Ser Glu Ile Met Glu Tyr Ser Val Leu Leu Pro Arg Thr
311         260             265             270
314 Leu Phe Gln Arg Thr Lys Gly Arg Ser Gly Glu Ala Glu Lys Arg Leu
315         275             280             285
318 Leu Leu Val Asp Phe Ser Ser Gln Ala Leu Phe Gln Asp Lys Asn Ser
319         290             295             300
322 Ser Gln Val Leu Gly Glu Lys Val Leu Gly Ile Val Val Gln Asn Thr
323 305             310             315             320
326 Lys Val Ala Asn Leu Thr Glu Pro Val Val Leu Thr Phe Gln His Gln
327             325             330             335
330 Leu Gln Pro Lys Asn Val Thr Leu Gln Cys Val Phe Trp Val Glu Asp
331             340             345             350
334 Pro Thr Leu Ser Ser Pro Gly His Trp Ser Ser Ala Gly Cys Glu Thr
335         355             360             365
338 Val Arg Arg Glu Thr Gln Thr Ser Cys Phe Cys Asn His Leu Thr Tyr
339         370             375             380
342 Phe Ala Val Leu Met Val Ser Ser Val Glu Val Asp Ala Val His Lys
343 385             390             395             400
346 His Tyr Leu Ser Leu Leu Ser Tyr Val Gly Cys Val Val Ser Ala Leu
347             405             410             415
350 Ala Cys Leu Val Thr Ile Ala Ala Tyr Leu Cys Ser Arg Val Pro Leu
351             420             425             430
354 Pro Cys Arg Arg Lys Pro Arg Asp Tyr Thr Ile Lys Val His Met Asn
355         435             440             445   ·
358 Leu Leu Leu Ala Val Phe Leu Leu Asp Thr Ser Phe Leu Leu Ser Glu
359         450             455             460
362 Pro Val Ala Leu Thr Gly Ser Glu Ala Gly Cys Arg Ala Ser Ala Ile
363 465             470             475             480
366 Phe Leu His Phe Ser Leu Leu Thr Cys Leu Ser Trp Met Gly Leu Glu
367             485             490             495
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371             500             505             510
374 Pro Gly Tyr Leu Leu Lys Leu Ser Ala Met Gly Trp Gly Phe Pro Ile
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**VERIFICATION SUMMARY**
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L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date